SEQUENCE LISTING

(1) GENERAL INFORMATION:

APPLICANT:
NAME: The Procter & Gamble Company
STREET: One Procter & Gamble Plaza
CITY: Cincinnati, OHIO
COUNTRY: USA
POSTAL CODE: 45202

TITLE OF INVENTION: Laundry detergent and/or fabric care compositions comprising a cellulase

NUMBER OF SEQUENCES: 1

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release # 1.0 Version 1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Gln Lys Pro Gly Glu Thr Lys Glu Val His Pro Gln
1 5 10

Leu Thr Thr Phe Arg Cys Thr Lys Arg Gly Gly Cys Lys Pro Ala Thr
15 20 25

Asn Phe Ile Val Leu Asp Ser Leu Ser His Pro Ile His Arg Ala Glu
30 35 40

Gly Leu Gly Pro Gly Gly Cys Gly Asp Trp Gly Asn Pro Pro Pro Lys
45 50 55 60

Asp Val Cys Pro Asp Val Glu Ser Cys Ala Lys Asn Cys Ile Met Glu
65 70 75

Gly Ile Pro Asp Tyr Ser Gln Tyr Gly Val Thr Thr Asn Gly Thr Ser

80 85 90

Leu Arg Leu Gln His Ile Leu Pro Asp Gly Arg Val Pro Ser Pro Arg
95 100 105

Val Tyr Leu Leu Asp Lys Thr Lys Arg Arg Tyr Glu Met Leu His Leu
110 115 120
Thr Gly Phe Glu Phe Thr Phe Asp Val Asp Ala Thr Lys Leu Pro Cys
125 130 135 140

Gly Met Asn Ser Ala Leu Tyr Leu Ser Glu Met His Pro Thr Gly Ala
145 150 155

Lys Ser Lys Tyr Asn Ser Gly Gly Ala Tyr Tyr Gly Thr Gly Tyr Cys
160 165 170

Asp Ala Gln Cys Phe Val Thr Pro Phe Ile Asn Gly Leu Gly Asn Ile
175 180 185

Glu Gly Lys Gly Ser Cys Cys Asn Glu Met Asp Ile Trp Glu Val Asn
190 195 200

Ser Arg Ala Ser His Val Val Pro His Thr Cys Asn Lys Lys Gly Leu
205 210 215 220

Tyr Leu Cys Glu Gly Glu Glu Cys Ala Phe Glu Gly Val Cys Asp Lys
225 230 235

Asn Gly Cys Gly Trp Asn Asn Tyr Arg Val Asn Val Thr Asp Tyr Tyr
240 245 250

Gly Arg Gly Glu Glu Phe Lys Val Asn Thr Leu Lys Pro Phe Thr Val
255 260 265

Val Thr Gln Phe Leu Ala Asn Arg Arg Gly Lys Leu Glu Lys Ile His
270 275 280

Arg Phe Tyr Val Gln Asp Gly Lys Val Ile Glu Ser Phe Tyr Thr Asn
285 290 295 300

Lys Glu Gly Val Pro Tyr Thr Asn Met Ile Asp Asp Glu Phe Cys Glu
305 310 315

Ala Thr Gly Ser Arg Lys Tyr Met Glu Leu Gly Ala Thr Gln Gly Met
320 325 330

Gly Glu Ala Leu Thr Arg Gly Met Val Leu Ala Met Ser Ile Trp Trp
335 340 345

Asp Gln Gly Gly Asn Met Glu Trp Leu Asp His Gly Glu Ala Gly Pro
350 355 360

Cys Ala Lys Gly Glu Gly Ala Pro Ser Asn Ile Val Gln Val Glu Pro
365 370 375 380

Phe Pro Glu Val Thr Tyr Thr Asn Leu Arg Trp Gly Glu Ile Gly Ser
385 390 395

Thr Tyr Gln Glu Val Gln Lys Pro Lys Pro Lys Pro Gly His Gly Pro
400 405 410

Arg Ser Asp
415